CLAIMS

1. A primer selected from the group consisting of at least 15 contiguous nucleotides of: TCTCAGTGGGCGTTCTTATG (SEQ ID NO. 1); TACCCCCTCAACTGCTAATA (SEQ ID NO. 2); TGTCTTCAGCATCTTATGCAG (SEQ ID NO. 3); CATGATTAATTACTGAAACAGAAAC (SEQ ID NO. 4); GCGGTTTTATTTGCATTAGC (SEQ ID NO. 5); TCCCGTCAACCTTCACTGTA (SEQ ID NO. 6); GCGGTTTTATTTGCATTAGT (SEQ ID NO. 7); GTACTCTTTTCCGGCCACT (SEQ ID NO. 8); ATGAAGTGTATATTGTTAAAGTGGA (SEQ ID NO. 9);AGCCACATATAAATTATTTCGT (SEQ ID NO. 10); ATGCTTAGTGCTGGTTTAGG (SEQ ID NO. 11); GCCTTCATCATTTCGCTTTC (SEQ ID NO. 12); GGTAAAATTGAGTTCTCTAAGTAT (SEQ ID NO. 13); CAGCAAATCCTGAACCTGACG (SEQ ID NO. 14); AGCTGCAAGTGCGGGTCTG (SEQ ID NO. 15); TACGGGTTATGCCTGCAAGTTCAC (SEQ ID NO. 16); CTACAGGTGAAGGTGGAATGG (SEQ ID NO. 17); ATTCCTCTCTTTCCTCTGCGG (SEQ ID NO. 18); TACCATCGCAAAAGCAACTCC (SEQ ID NO. 19); GTCGGCAACGTTAGTGATACC (SEQ ID NO. 20); CCCCCTGGACGAAGACTGAC (SEQ ID NO. 21) and ACCGCTGGCAACAAAGGATA (SEQ ID NO. 22) and combinations thereof.

2. A kit comprising at least one primer selected from the group consisting of at least 15 contiguous nucleotides of: TCTCAGTGGGCGTTCTTATG (SEQ ID NO. 1); TACCCCCTCAACTGCTAATA (SEQ ID NO. 2); TGTCTTCAGCATCTTATGCAG (SEQ ID NO. 3); CATGATTAATTACTGAAACAGAAAC (SEQ ID NO. 4); GCGGTTTTATTTGCATTAGC (SEQ ID NO. 5); TCCCGTCAACCTTCACTGTA (SEQ ID NO. 6); GCGGTTTTATTTGCATTAGT (SEQ ID NO. 7); AGTACTCTTTTCCGGCCACT (SEQ ID NO. 8); ATGAAGTGTATATTGTTAAAGTGGA (SEQ ID NO. 9); AGCCACATATAAATTATTTCGT (SEQ ID NO. 10); ATGCTTAGTGCTGGTTTAGG (SEQ ID NO. 11); GCCTTCATCATTTCGCTTTC (SEQ ID NO. 12); GGTAAAATTGAGTTCTCTAAGTAT (SEQ ID NO. 13); CAGCAAATCCTGAACCTGACG (SEQ ID NO. 14); AGCTGCAAGTGCGGGTCTG (SEQ ID NO. 15); TACGGGTTATGCCTGCAAGTTCAC (SEQ ID NO. 16) ; CTACAGGTGAAGGTGGAATGG (SEQ ID NO. 17); ATTCCTCTCTTTCCTCTGCGG (SEQ ID NO. 18); TACCATCGCAAAAGCAACTCC (SEQ ID NO. 19); GTCGGCAACGTTAGTGATACC (SEQ ID NO. 20); CCCCCTGGACGAAGACTGAC (SEQ ID NO. 21) and ACCGCTGGCAACAAAGGATA (SEQ ID NO. 22) and combinations thereof.

3. A method of detecting the presence or absence of *E. coli* virulence-related genes in a sample comprising:

adding the sample to an amplification mixture including at least one pair of primers selected from the group consisting of at least 15 contiguous nucleotides of: TCTCAGTGGGCGTTCTTATG (SEQ ID NO. 1) and TACCCCCTCAACTGCTAATA (SEQ ID NO. 2); TGTCTTCAGCATCTTATGCAG (SEQ ID NO. 3) and CATGATTAATTACTGAAACAGAAAC (SEQ ID NO. 4); GCGGTTTTATTTGCATTAGC (SEQ ID NO. 5) and TCCCGTCAACCTTCACTGTA (SEQ ID NO. 6); GCGGTTTTATTTGCATTAGT (SEQ ID NO. 7) and AGTACTCTTTTCCGGCCACT (SEQ ID NO. 8); ATGAAGTGTATATTGTTAAAGTGGA (SEQ ID NO. 9) and AGCCACATATAAATTATTTCGT (SEQ ID NO. 10); ATGCTTAGTGCTGGTTTAGG (SEQ ID NO. 11) and GCCTTCATCATTTCGCTTTC (SEQ ID NO. 12); GGTAAAATTGAGTTCTCTAAGTAT (SEQ ID NO. 13) and CAGCAAATCCTGAACCTGACG (SEQ ID NO. 14); AGCTGCAAGTGCGGGTCTG (SEQ ID NO. 15) and TACGGGTTATGCCTGCAAGTTCAC (SEQ ID NO. 16) ; CTACAGGTGAAGGTGGAATGG (SEQ ID NO. 17) and ATTCCTCTCTTTCCTCTGCGG (SEQ ID NO. 18); TACCATCGCAAAAGCAACTCC (SEQ ID NO. 19) and GTCGGCAACGTTAGTGATACC (SEQ ID NO. 20); CCCCCTGGACGAAGACTGAC (SEQ ID NO. 21) and ACCGCTGGCAACAAAGGATA (SEQ ID NO. 22) and combinations thereof;

incubating the amplification mixture under conditions which promote DNA amplification; and

identifying the amplification products.